

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/575,362
Source: IFWP
Date Processed by STIC: 04/25/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/575, 362

CRF Edit Date: 04/25/2006
Edited by: DA

___ **Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line**

___ **Corrected the SEQ ID NO. Sequence numbers edited were:**

___ **Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:**

/ Deleted: / invalid beginning/end-of-file text ; ___ page numbers

___ **Inserted mandatory headings/numeric identifiers, specifically:**

___ **Moved responses to same line as heading/numeric identifier, specifically:**

___ **Other:**



IFWP

RAW SEQUENCE LISTING

DATE: 04/25/2006

PATENT APPLICATION: US/10/575,362

TIME: 14:55:09

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\04252006\J575362.raw

3 <110> APPLICANT: Bayer HealthCare AG
 5 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with N-Acetylated
 6 Alpha-Linked Acidic Dipeptidase 2 (NAALADASE 2)
 8 <130> FILE REFERENCE: BHC 03 01 004
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/575,362
 C--> 10 <141> CURRENT FILING DATE: 2006-04-11
 10 <160> NUMBER OF SEQ ID NOS: 5
 12 <170> SOFTWARE: PatentIn version 3.1
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 3152
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 19 <400> SEQUENCE: 1

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22	atgggtgggct	ggtttattaa	gcctctcaaa	gaaacaacca	cttctgtgcy	ctatcatcaa	180
23	agtatacggg	ggaaactggg	atccgaaatg	aaagctgaaa	acatcaaatc	atttcttcgt	240
24	tcttttacaa	agcttcctca	tctggcagga	acagaacaaa	atttcttgct	tgccaagaaa	300
25	atccaaaccc	agtgggaagaa	atttggaacta	gattcagcca	agttgggttca	ttatgatgtc	360
26	ctcttatctt	accccaatga	gacaaatgcc	aactatatat	cgattgtgga	tgaacatgaa	420
27	actgagattt	tcaaaacatc	ataccttgaa	ccaccaccag	atggctatga	gaatgttaca	480
28	aatattgtgc	caccatataa	tgtcttctca	gccccaggca	tgccagaggg	agatcttgta	540
29	tatgtgaact	atgctcgcac	tgaagacttt	ttcaaaactag	aaagagagat	gggcatcaac	600
30	tgtactggga	agattgttat	tgaagatat	ggaaaaatct	tcagaggaaa	taaagttaaa	660
31	aatgccatgt	tagcaggagc	cataggaatc	atcttgta	cagatccagc	tgactacttt	720
32	gctcctgagg	tacagccata	tcccaaagga	tggaaatctt	ctggaactgc	agcccagaga	780
33	ggaaatgtgt	taaatttgaa	tgggtgctgg	gacccactca	ctccaggcta	tccagcaaaa	840
34	gaatacactt	tcagacttga	tgttgaagaa	ggagtgggaa	tccccgaat	acctgtacat	900
35	cccattggat	ataatgatgc	agaaatatta	ttacgctact	tgggaggaat	tgctccacca	960
36	gataagagtt	ggaaggaggc	ccttaatgtg	agttatagta	tcggacctgg	ctttacaggg	1020
37	agtgattctt	tcaggaaggt	tagaatgcat	gtttataaca	tcaataaaat	tacaaggatt	1080
38	tacaatgtag	ttggaactat	cagaggatct	gtggaacctg	acaggatatg	tattctggga	1140
39	ggtcaccggg	actcctgggt	atttggagct	attgacccaa	ccagtggggg	tgctgttttg	1200
40	caagaaattg	cccggagttt	tggaaaactg	atgagtaaag	gctggagacc	tagaagaact	1260
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43	atagaaggca	attatactct	cagagttgac	tgtactcccc	ttctttacca	attagtgtat	1440
44	aaactgacaa	aagagatccc	cagccctgat	gatgggtttg	agagtaaata	actgtatgaa	1500
45	agctggttgg	aaaaagaccc	ttcacctgaa	aataaaaatt	tgcttagaat	caataagctg	1560
46	ggatctggaa	gtgactttga	agcttatttt	cagagacttg	gaattgcttc	aggcagagcc	1620
47	cgttacacta	agaataagaa	aacagataag	tacagcagct	accagtgta	ccacacaatt	1680
48	tatgagacat	ttgaattggg	agagaaat	tatgacccca	catttaaaaa	acaactttct	1740
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Input Set : A:\pto.da.txt

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51 aagaaacatg atcaacaatt aacagaccat ggagtatcat ttgactcctt attttctgct 1920
52 gtgaaaaact tctcagaggc tgcttcagat tttcataaac gacttataca agttgatctt 1980
53 aacaatccca ttgcagtgag aatgatgaat gaccaactga tgctcctgga aagagcattc 2040
54 atcgatcctc ttggtttacc aggaaagctg ttctataggc acatcatatt tgctccaagt 2100
55 agccacaaca aatatgctgg agaatcattt cctggaatct atgatgctat ctttgatatt 2160
56 gaaaataaag ccaactctcg tttggcctgg aaagaagt agaaacatat ttctattgca 2220
57 gcttttaciaa ttcaagcagc agcaggaact ctgaagaag tattatagaa ggtctcaagt 2280
58 ggctagccat taaagggtgtt gctaaaagtc tgaggataaa attcaccttt ctgataactt 2340
59 atgaagccag ggtgttctaa actcttttca tgtcatgttt tgattatagg ctttggctct 2400
60 ttcattctgca aagccttttt tttttttgct ctttaaaagt taataattat attagcaaag 2460
61 tgtaaatcta atgaagtaaa aaactcctgt gtggcagaaa gtaaaagaaa attccctaaa 2520
62 ttatagcaag gaacatgaat tctcagacat tgtgagtgtg ggaatgtaaa atggtaaaat 2580
63 cacttttgaa aacagtttgg cagtttccta taaagttaaa catacacttt tacttttagga 2640
64 ctccagaatt ccacttctag ttattttattc aagagaagga aaaacaatga tcacagcaat 2700
65 acttgtagc atgttcattg caacttaaaa gcgtaaaaac cccaaatgtc catccacaga 2760
66 cgaatgtata aactgtggtt tccattacac aatagactac ttactactca gcaataaaaa 2820
67 tgaagtaact ttcaataaat gcaatattat tggcagacat tgttgaagga aaaagccag 2880
68 acaaaacaact acataaaaata tgtttctatt taagtgaagt ggcaaaactaa tctgtagtgt 2940
69 taaaaattag attagtgtt gcctgggcca agtggcaggt tggggaggat ggctgcaaay 3000
70 aagtatgagg aaactttctc caatagatga gaattttccg tatcttgatc tgagtggcaa 3060
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72 attataaaaa aaaaaaaaaa aagggcggcc gc 3152
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 740
76 <212> TYPE: PRT
77 <213> ORGANISM: Homo sapiens
79 <400> SEQUENCE: 2
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81 1 5 10 15
82 Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp Phe Ile Lys
83 20 25 30
84 Pro Leu Lys Glu Thr Thr Thr Ser Val Arg Tyr His Gln Ser Ile Arg
85 35 40 45
86 Trp Lys Leu Val Ser Glu Met Lys Ala Glu Asn Ile Lys Ser Phe Leu
87 50 55 60
88 Arg Ser Phe Thr Lys Leu Pro His Leu Ala Gly Thr Glu Gln Asn Phe
89 65 70 75 80
90 Leu Leu Ala Lys Lys Ile Gln Thr Gln Trp Lys Lys Phe Gly Leu Asp
91 85 90 95
92 Ser Ala Lys Leu Val His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Glu
93 100 105 110
94 Thr Asn Ala Asn Tyr Ile Ser Ile Val Asp Glu His Glu Thr Glu Ile
95 115 120 125
96 Phe Lys Thr Ser Tyr Leu Glu Pro Pro Pro Asp Gly Tyr Glu Asn Val
97 130 135 140
98 Thr Asn Ile Val Pro Pro Tyr Asn Ala Phe Ser Ala Gln Gly Met Pro
99 145 150 155 160
100 Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe

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101          165          170          175
102 Lys Leu Glu Arg Glu Met Gly Ile Asn Cys Thr Gly Lys Ile Val Ile
103          180          185          190
104 Ala Arg Tyr Gly Lys Ile Phe Arg Gly Asn Lys Val Lys Asn Ala Met
105          195          200          205
106 Leu Ala Gly Ala Ile Gly Ile Ile Leu Tyr Ser Asp Pro Ala Asp Tyr
107          210          215          220
108 Phe Ala Pro Glu Val Gln Pro Tyr Pro Lys Gly Trp Asn Leu Pro Gly
109 225          230          235          240
110 Thr Ala Ala Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala Gly Asp
111          245          250          255
112 Pro Leu Thr Pro Gly Tyr Pro Ala Lys Glu Tyr Thr Phe Arg Leu Asp
113          260          265          270
114 Val Glu Glu Gly Val Gly Ile Pro Arg Ile Pro Val His Pro Ile Gly
115          275          280          285
116 Tyr Asn Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro
117          290          295          300
118 Pro Asp Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly
119 305          310          315          320
120 Pro Gly Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val
121          325          330          335
122 Tyr Asn Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile
123          340          345          350
124 Arg Gly Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg
125          355          360          365
126 Asp Ser Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val
127          370          375          380
128 Leu Gln Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp
129 385          390          395          400
130 Arg Pro Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe
131          405          410          415
132 Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu
133          420          425          430
134 Gln Glu Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly
135          435          440          445
136 Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val
137          450          455          460
138 Tyr Lys Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser
139 465          470          475          480
140 Lys Ser Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn
141          485          490          495
142 Lys Asn Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu
143          500          505          510
144 Ala Tyr Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr
145          515          520          525
146 Lys Asn Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val Tyr His Thr
147          530          535          540
148 Ile Tyr Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe
149 545          550          555          560

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150 Lys Lys Gln Leu Ser Val Ala Gln Leu Arg Gly Ala Leu Val Tyr Glu
151          565          570          575
152 Leu Val Asp Ser Lys Ile Ile Pro Phe Asn Ile Gln Asp Tyr Ala Glu
153          580          585          590
154 Ala Leu Lys Asn Tyr Ala Ala Ser Ile Tyr Asn Leu Ser Lys Lys His
155          595          600          605
156 Asp Gln Gln Leu Thr Asp His Gly Val Ser Phe Asp Ser Leu Phe Ser
157          610          615          620
158 Ala Val Lys Asn Phe Ser Glu Ala Ala Ser Asp Phe His Lys Arg Leu
159 625          630          635          640
160 Ile Gln Val Asp Leu Asn Asn Pro Ile Ala Val Arg Met Met Asn Asp
161          645          650          655
162 Gln Leu Met Leu Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro
163          660          665          670
164 Gly Lys Leu Phe Tyr Arg His Ile Phe Ala Pro Ser Ser His Asn
165          675          680          685
166 Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Ile Phe Asp
167          690          695          700
168 Ile Glu Asn Lys Ala Asn Ser Arg Leu Ala Trp Lys Glu Val Lys Lys
169 705          710          715          720
170 His Ile Ser Ile Ala Ala Phe Thr Ile Gln Ala Ala Ala Gly Thr Leu
171          725          730          735
172 Lys Glu Val Leu
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176 <211> LENGTH: 20
177 <212> TYPE: DNA
178 <213> ORGANISM: artificial sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: forward primer
183 <400> SEQUENCE: 3
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187 <211> LENGTH: 20
188 <212> TYPE: DNA
189 <213> ORGANISM: artificial sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: reverse primer
194 <400> SEQUENCE: 4
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197 <210> SEQ ID NO: 5
198 <211> LENGTH: 22
199 <212> TYPE: DNA
200 <213> ORGANISM: artificial sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: probe
205 <400> SEQUENCE: 5
206 ctgctgcgct ggcatttttc ct

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20

20

22

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/575,362

DATE: 04/25/2006

TIME: 14:55:10

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\04252006\J575362.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

**Raw Sequence Listing before editing
(for reference only)**



IFWP

RAW SEQUENCE LISTING

DATE: 04/24/2006

PATENT APPLICATION: US/10/575,362

TIME: 16:24:48

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575362.raw

3 <110> APPLICANT: Bayer HealthCare AG

5 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases

Associated with N-Acetylated

6 Alpha-Linked Acidic Dipeptidase 2 (NAALADASE 2)

8 <130> FILE REFERENCE: BHC 03 01 004

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/575,362

C--> 10 <141> CURRENT FILING DATE: 2006-04-11

10 <160> NUMBER OF SEQ ID NOS: 5

12 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

197 <210> SEQ ID NO: 5

198 <211> LENGTH: 22

199 <212> TYPE: DNA

200 <213> ORGANISM: artificial sequence

202 <220> FEATURE:

203 <223> OTHER INFORMATION: probe

205 <400> SEQUENCE: 5

206 ctgctgcgct ggcattttc ct

E--> 208 bhc 03 1 003

E--> 210 - 5 -

E--> 213 bhc 03 1 003

E--> 215 - 1 -

Does Not Comply
Corrected Diskette Needed

Cp9-1)

22

deleted

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/575,362

DATE: 04/24/2006

TIME: 16:24:49

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575362.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:208 M:254 E: No. of Bases conflict, LENGTH:Input:3 Counted:25 SEQ:5
L:208 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=5
M:112 Repeated in SeqNo=5
L:215 M:252 E: No. of Seq. differs, <211> LENGTH:Input:22 Found:28 SEQ:5